RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

Source:

Date Processed by STIC:

10751,235

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/18/2004

PATENT APPLICATION: US/10/751,235

TIME: 12:20:26

Input Set : A:\08604~2.txt

Output Set: N:\CRF4\11182004\J751235.raw

```
3 <110> APPLICANT: DellaPenna, Dean
         Tian, Li
             Kim, Joonyul
     7 <120> TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering
Carotenoid
     8
             Metabolism in Plants
    10 <130> FILE REFERENCE: MSU-08604
    12 <140> CURRENT APPLICATION NUMBER: 10/751,235
    13 <141> CURRENT FILING DATE: 2004-01-02
    15 <160> NUMBER OF SEQ ID NOS: 74
    17 <170> SOFTWARE: PatentIn version 3.2
    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 77
    21 <212> TYPE: PRT
    22 <213> ORGANISM: Arabidopsis thaliana
    24 <400> SEQUENCE: 1
    26 Leu Gln Pro Tyr Ala Glu Asp Gly Ser Ala Val Asn Met Glu Ala Lys
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                                           10
    30 Phe Ser Gln Met Thr Leu Asp Val Ile Gly Leu Ser Leu Phe Asn Tyr
                   20
    34 Asn Phe Asp Ser Leu Thr Thr Asp Ser Pro Val Ile Glu Ala Val Tyr
    38 Thr Ala Leu Lys Glu Ala Glu Leu Arg Ser Thr Asp Leu Leu Pro Tyr
    39
                               55
    42 Trp Lys Ile Asp Ala Leu Cys Lys Ile Val Pro Arg Gln
    43 65
    46 <210> SEQ ID NO: 2
    47 <211> LENGTH: 77
    48 <212> TYPE: PRT
    49 <213> ORGANISM: Arabidopsis thaliana
    51 <400> SEQUENCE: 2
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    54 1
    57 Phe Ser Arg Leu Thr Leu Asp Ile Ile Gly Lys Ala Val Phe Asn Tyr
    61 Asp Phe Asp Ser Leu Thr Asn Asp Thr Gly Val Ile Glu Ala Val Tyr
    65 Thr Val Leu Arg Glu Ala Glu Asp Arg Ser Val Ser Pro Ile Pro Val
    66
    69 Trp Asp Ile Pro Ile Trp Lys Asp Ile Ser Pro Arg Gln
    70 65
    73 <210> SEQ ID NO: 3
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74 <211> LENGTH: 84 75 <212> TYPE: PRT

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Input Set : A:\08604~2.txt

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```
76 <213> ORGANISM: Arabidopsis thaliana
78 <400> SEQUENCE: 3
80 Glu Lys Leu Ile Arg Glu Lys Glu Thr Ser Ser Gly Glu Asp Thr Ile
                                       . 10
84 Glu Leu Asp Leu Glu Ala Glu Phe Ser Ser Leu Ala Leu Asp Ile Ile
88 Gly Leu Ser Val Phe Asn Tyr Asp Phe Gly Ser Val Thr Lys Glu Ser
                               40
92 Pro Val Ile Lys Ala Val Tyr Gly Thr Leu Phe Glu Ala Glu His Arg
96 Ser Thr Phe Tyr Phe Pro Tyr Trp Asn Phe Pro Pro Ala Arg Trp Ile
100 Val Pro Arg Gln
104 <210> SEQ ID NO: 4
105 <211> LENGTH: 539
106 <212> TYPE: PRT
107 <213> ORGANISM: Arabidopsis thaliana
109 <400> SEQUENCE: 4
111 Met Glu Ser Ser Leu Phe Ser Pro Ser Ser Ser Tyr Ser Ser Leu
115 Phe Thr Ala Lys Pro Thr Arg Leu Leu Ser Pro Lys Pro Lys Phe Thr
                20
119 Phe Ser Ile Arg Ser Ser Ile Glu Lys Pro Lys Pro Lys Leu Glu Thr
123 Asn Ser Ser Lys Ser Gln Ser Trp Val Ser Pro Asp Trp Leu Thr Thr
                            55
127 Leu Thr Arg Thr Leu Ser Ser Gly Lys Asn Asp Glu Ser Gly Ile Pro
                        70
131 Ile Ala Asn Ala Lys Leu Asp Asp Val Ala Asp Leu Leu Gly Gly Ala
135 Leu Phe Leu Pro Leu Tyr Lys Trp Met Asn Glu Tyr Gly Pro Ile Tyr
139 Arg Leu Ala Ala Gly Pro Arg Asn Phe Val Ile Val Ser Asp Pro Ala
143 Ile Ala Lys His Val Leu Arg Asn Tyr Pro Lys Tyr Ala Lys Gly Leu
        130
                            135
147 Val Ala Glu Val Ser Glu Phe Leu Phe Gly Ser Gly Phe Ala Ile Ala
                        150
                                            155
151 Glu Gly Pro Leu Trp Thr Ala Arg Arg Arg Ala Val Val Pro Ser Leu
                    165
155 His Arg Arg Tyr Leu Ser Val Ile Val Glu Arg Val Phe Cys Lys Cys
                180
                                    185
159 Ala Glu Arg Leu Val Glu Lys Leu Gln Pro Tyr Ala Glu Asp Gly Ser
                                200
163 Ala Val Asn Met Glu Ala Lys Phe Ser Gln Met Thr Leu Asp Val Ile
                                                220
        210
                            215
167 Gly Leu Ser Leu Phe Asn Tyr Asn Phe Asp Ser Leu Thr Thr Asp Ser
                        230
                                            235
171 Pro Val Ile Glu Ala Val Tyr Thr Ala Leu Lys Glu Ala Glu Leu Arg
```

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Input Set : A:\08604~2.txt
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	172					245					250		•			255			
	175	Ser	Thr	Asp	Leu	Leu	Pro	Tyr	Trp	Lys	Ile	Asp	Ala	Leu	Cys	Lys	Ile		
	176				260					265					270				
	179	Val	Pro	Arg	Gln	Val	Lys	Ala	Glu	Lys	Ala	Val	Thr	Leu	Ile	Arg	Glu		
	180			275					280					285				• •	
		Thr		Glu	Asp	Leu	Ile		Lys	СĀ	Lys	Glu		Val	Glu	Arg	Glu		•
	184		290		O_			295			_		300						
			Glu	Arg	Ile	Asn			Glu	Tyr	Val		Asp	Ala	Asp	Pro			
		305	_		_2	_*.	310					315		2	_		320		
		Ile	Leu	Arg	Phe			Ala	Ser	Arg		Gļu	Val	Ser	Ser	Val	Gln		
	192	7	7			325		0	**		330	70.71	01	***		335	ml	•	
		ьeu	Arg	Asp		цеu	ьeu	ser	мес		vaı	Ата	GTA	HIS		Thr	rnr		
	196	C1	Corr	1707	340	mb x	Пост	The	T 011	345	Ton	του.	Cox	Tira	350	Com	Com		
	200	GIA	Ser	355	ьeu	TIIT	тър	1111.	360	TYL	тей	пéй	ser	3.65	ASII	ser	Ser		
		ηja	T.011		Tuc	λla	G] n	Clui		T-T	Acn	λνα	Val.		Glu	Gly	77.20		
	203	Ата	370	Arg	цур	MIG	Gili	375	Ģīu	vai	veĥ	Arg	380	цец	Giu	СТУ	AIG		
		Agn		Δla	Phe	Ġ111	Asn		Livs	Glu	T.eu	Lvs		τĺο	Thr	Arg	Cvs		
	208			111.0	1110		390	,	цу	0.10	ب پ	395	-,1 -	110	+111	ģ	400		
			Asn	Glu	Ser	Met		Leu	Tvr	Pro	His		Pro	Val	Leu	Ile			
	212					405					410					415			
		Arg	Ala	Gln	Val		Asp	Ile	Leu	Pro	Gly	Asn	Tyr	Lys	Val	Asn	Thr		
	216	J			420		-			425	•	•	-	• .	430				
	219	Gly	Gln	Asp	Ile	Met	Ile	Ser	Val	Tyr	Asn	Ile	His	Arg	Ser	Ser	Glu		
	220			435					440					445					
	223	Val	Trp	Glu	Lys	Ala	Glu	Glu	Phe	Leu	Pro	Glu	Arg	Phe	Asp	Ile	Asp		
-	224		450°		. (455				G 1 701	460	2 41.00	/= -24 -				
	227	Gly	Ala	Ile	Pro	Asn	Glu	Thr	Asn	Thr	Asp	Phe	Lys	Phe	Ile	Pro	Phe		
	228						470					475	-				480	٠.	
			Gly	Gly	Pro	-	Lys	Cys	Val	Gly		Gln	Phe	Ala	Leu	Met	Glu		
	232-	•				485	_ =				490		_			495			
		Ala	Ile	Val		Leu	Ala	Val	Phe		Gin	Arg	Leu	Așn		Glu	Leu	•	
	236	** . 3			500	m1	- 1 -			505	ml	~1	77.	m1	510	TT -	ml		
		vai	Pro	_	GIN	Tnr	ше	ser		Inr	Tnr	GIA	Ата		тте	His	Thr		•
	240	The	7 00	515	T 011	Me ran	Mot	T.rra	520	Cox	Cln.	7\ ~~~ ~		525					
	244	TIIL	530	GIY	neu	тÄт	Met.	_	val	Ser	Gln	Arg							
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																	ttgag		120
																	ccgat		180
																	tacca	-	240
							_						_		-		tacct		300
																	gtaat		360
																	agtac		420
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26	7 gctaaaggct	taqtcqctqa	agtctctgaa	tttctatttg	gttdgggttt	cgctatcgct	480
	gaaggacctc						540
	L ttgtggaagt						600
	3 tccaatcttc						660
	cggtggttcc						720
	7 aatgtgcága					· ·	780
	atatggaagc	7					840
	l acaatttcga						900
	acaactcega aagaagctga			-			960
							1020
	ttttctgtgg						1020
	7 ttgtttttt						
	ggctgtaact						1140
	L cgaaagagaá						1200
	3 cctgcgtttc						1260
	caaatttggc						1320
	7 gtatcaagtg						1380
	actggatctg						1440
30	l tactttgcta	tgctagagaa	tttacttgga	tgggagcttc	tctgttctca	tttacctctt	1500
30	3 caaattctct	atgttcatag	aactcatctg	cattaaggaa	agcacaagaa	gaagtagaca	1560
30	gagtgttaga	aggaagaaac	ccggctttcg	aggatataaa	ggagttgaag	tacatcactc	1620
30	7 gttgtataaa	cgagtcaatg	cgtctctatc	ctcatcctcc	tgtaagcaat	caagctcatc	1680
30) tctctaatta	ttcatgaact	aaattttctg	attgatttgt	ttcctggtag	gtcttgataa	1740
	L gaagagetea						1800
31	3 ttatgatttc	agtctataac	atccatcgtt	cttccgaggt	acagttctct	tccttctctc	1860
	gtccatagta						1920
	7 atatctaacc						1980
	gttgtttgtt			_	the second secon	and the second of the second	2040
	l catagatggc						2100
	atcttttgac						2160
	gattttcttt						2220
	7 atcagtttgc						2280
	ttgagetggt						2340
	l atgtatgcca						2400
	attccaattt						2460
		Ciciaaigci	gacacccca	acccaggga	ccgcacacga	aggegageea	2467
	5 aaggtaa 3 <210> SEQ 3	TD NO. 6					2407
	9 <211> SEQ .			5.'		•	
) <212> TYPE		· · · · · · · · · · · · · · · · · · ·				
	L <213> ORGAI		opsis that:	Lana			
	3 <400> SEQUI						
	l cctggtcaag			_			60
	gttcatccac						120
	acactcgaga						180
) aagacgataa						240
	tgaggccggg						300
	gaagetteet						360
	aacaaaaaaa						420
358	acctcataaa	cttgaaaggt	gcatttatac	agcacatcat	tgtaaaccta	atatcagtaa	480
	ctatgaaccc						540
							*

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	362	tcaaatatat	cattatagct	caacaaacta	cacaacaaca	agatttcctt	aatcgctaac	600
	364	agacctaatg	tetggateae	gcaatttcat	caataacata'	tgaatcagat	ggcaaaaaat	660
	366	tcgcaaaatc	ataccagaaa	ttgaacatcg	tttctagaat	tcgccgacta	acgaaaggaa	720
					cttcctacca			780
	370	tttacagaaa	cagagtttac	agagtttcaa	agaaaattcg	atcttctctg	tttcgtttca	840
•		_		7	atacgaggag			900
					tccttatcca			960
					cttcgaaaag			1020
					ttctctcttc			1080
					catcagatcc			1140
					atcatgggtc			1200
				·	cgacgagtca		*	1260
					aggtgctctc			1320
					cgctgctggt			. 1380
					gaggaattat			1440
					ttcgggtttc			1500
					aattttgaag			1560
			,		ctaattttag	•		1620
					acataggcga			1680
					gtggagagag			1740
					gaagacggaa			1800
					gggttgtctc			1860
					gctgtttaca			1920
					aaggcaagtt			1980
					gttaattgag			2040
					gacaggtgaa			2100
					ctaagtgtaa			2160
					atgatgctga			2220
					ttttccttaa			2280
					gcattgtgag			2340
					cgtagcgggt			2400
					ggtaccttaa			2460
					ctgttctcat			2520
					gcacaagaag			2580
	430	ggaagaaacc	cggctttcga	ggatataaag	gagttgaagt	acatcactcg	ttgtataaac	2640
	432	gagtcaatgc	gtctctatcc	tcatcctcct	gtaagcaatc	aagctcatct	ctctaattat	2700
					tcctggtagg			2760
	436	gttcctgaca	ttcttcctgg	gaactataag	gtcaataccg	gacaagacat	tatgatttca	2820
					cagttctctt			2880
	440	aacatagggg	agcctaatcc	ttctcttcaa	tgatctttgt	gtggttcgga	tatctaaccg	2940
	442	gagtggacat	tcctagtatt	acattcatgc	ccacatttct	tatgtgtttg	ttgtttgtta	3,000
	444	ttccaaaggt	atgggaaaaa	gctgaggaat'	ttctgcctga	acgattcgac	atagatggcg	3060
	446	caatccctaa	cgaaacaaac	actgatttca	agtaaactca	gtagaacaca	tcttttgaca	3120
	448	caaactactg	aatcaagatt	agtggttttg	attagggaat	ttaaaagatg	attttcttt	3180
	450	ttcaccagat	tcatcccatt	cagtggaggg	cctagaaaat	gtgtaggcga	tcagtttgca	3240
	452	ttgatggagg	caattgtggc	actcgcggtg	tttcttcagc	ggttaaacgt	tgagctggtt	3300
					gcaaccatac			3360
					gtctgttttg			3420
					tgtatatgaa			3480

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/10/751,235

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 1,3,4,6

Seq#:14; Xaa Pos. 2,3,5,6,7,9

Seq#:17; Xaa Pos. 529
Seq#:23; N Pos. 1587

VERIFICATION SUMMARY

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Input Set : A:\08604~2.txt

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L:579 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE: L:584 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:

L:657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0

L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:528 L:1441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:1560

L:4278 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (58) SEQUENCE: